

Structural basis for stable DNA complex formation by the caspase-activated DNase

Reh S., Korn C., Gimadutdinow O., Meiss G.

Kazan Federal University, 420008, Kremlevskaya 18, Kazan, Russia

Abstract

We describe a structural model for DNA binding by the caspase-activated DNase (CAD). Results of a mutational analysis and computational modeling suggest that DNA is bound via a positively charged surface with two functionally distinct regions, one being the active site facing the DNA minor groove and the other comprising distal residues close to or directly from helix $\alpha 4$, which binds DNA in the major groove. This bipartite protein-DNA interaction is present once in the CAD/inhibitor of CAD heterodimer and repeated twice in the active CAD dimer. © 2005 by The American Society for Biochemistry and Molecular Biology, Inc.

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